

Serial No. 09/538,396  
Group Art Unit: 1638

### REMARKS

Reconsideration of the present application is respectfully requested. Claims 2-8, and 12-15 are pending. Claims 9-11 have been cancelled as belonging to a non-elected invention. The right to pursue these claims in a continuing application is reserved. No change of inventorship is necessary. Claim 1 has been cancelled and rewritten as new claims 12-15. Claims 2-4 have been amended to correct dependency. Support for these claims is found in the claims as originally filed, and throughout the specification. No new matter has been added.

Applicant has amended the specification to delete references to Internet hyperlinks.

The marked up version of these amendments is found on a separate sheet attached to this amendment and titled "**Version with Markings to Show Changes Made.**" It is respectfully requested that the amendments be entered.

### **Election/Restriction**

The Examiner has issued a restriction requirement, and has required election of either the invention of Group I (Claims 1-8) or Group II (Claims 9-11). Applicants hereby affirm the election to prosecute the claims of Group I, with traverse as filed 8/31/01. Applicants expressly reserve the right to file a divisional applications relating to and claiming the inventions of Group II and/or Group III. No change of inventorship is required due to this election of Group I.

### **Rejections under 35 U.S.C. §101:**

Claims 1-8 are rejected under 35 U.S.C. §101 as not having either a credible asserted utility or a well-established utility. Claim 1 has been cancelled and rewritten as claims 12-15, the rejection will be discussed as it applies to these claims.

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The Examiner asserts that "No function of said polynucleotides are recited."

Applicants have rewritten claim 1 as new claims 12-15. New claims 12 and 13 now recite "wherein the polynucleotide encodes a polypeptide with Rad50 activity." New claim 15 is dependent on new claim 12, so also requires that 30 contiguous nucleotides come from a polynucleotide which encodes a polypeptide with Rad50 activity. New claim 14 is directed to polynucleotides which hybridize to SEQ ID NO: 1. Therefore, new claims 12-14 and dependent claims 2-8, and 15 do recite the function of the polynucleotides.

The Examiner asserts "Applicants assert that a polynucleotide having 80% sequence identity to SEQ ID NO: 1 would have Rad50 activity. However it is unclear what would be the utility of said polynucleotide if the 20% lack of identity falls in a region crucial for the Rad50 activity."

Applicants have rewritten claim 1 as new claims 12-15. This rejection will be discussed as it applies to new claim 12. In the preamble, Claim 12 recites "An isolated polynucleotide encoding a polypeptide with Rad50 activity ". Therefore, only polynucleotides with 80% sequence identity to SEQ ID NO: 1, which also encode a polypeptide with Rad50 activity are claimed. Further, not all embodiments must have utility for the invention as a whole to have utility. Inoperable embodiments of the claimed invention do not eliminate the utility of the operable embodiments. As it is stated in the MPEP 2107 II, page 2100-25: "... as the Federal Circuit has stated, '[t]o violate [35 U.S.C.] 101 the claimed device must be totally incapable of achieving a useful result.' *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571, 24 USPQ2d 1401, 1412 (Fed. Cir. 1992)".

The Examiner states "No data that relates SEQ ID NO: 1 or SEQ ID NO: 2 to Rad50 activity has been shown."

Applicants respectfully disagree, page 1, line 15 – page 2, line 15 of the specification clearly details the well-established activity and features of Rad50 polypeptides. Rad50 has been shown to be involved in DNA recombination and

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repair, the present invention proposes to use the well established activity of Rad50 to improve transformation efficiency in plants, therefore establishing specific and substantial utility for the present invention. Page 2, lines 18-25, and in Example 4 on pages 62-64, of the specification discuss the structural features shared by SEQ ID NO:2 of the present invention and other known Rad50 proteins, including the predicted molecular weight, the presence of two ATP-binding sites (Walker boxes), nuclear localization signals, heptad repeats, and leucine zippers. In Appendix A, Applicants submit a multiple sequence alignment of SEQ ID NO: 2 with several other Rad50 proteins. Identical and conserved amino acids, relative to SEQ ID NO: 2, are highlighted. The multiple sequence alignment illustrates the extensive homology, over the entire length of SEQ ID NO: 2, to other Rad50 proteins.

The Examiner asserts "However, the state of the art as exemplified by Bork et al suggests that a 31.7% of sequence identity of Applicant's SEQ ID NO: 2 with the known protein is insufficient to predictably determine the function of Applicant's protein."

The identification of SEQ ID NO: 1 and SEQ ID NO: 2 as Rad50 polynucleotide and polypeptide respectively, is not based merely on percent sequence identity alone, but is based on an analysis of several features, such as molecular weight, and sequence homology to known conserved domains contained in Rad50. These features include the presence and positioning of ATP-binding sites, nuclear localization signals, heptad repeats, and leucine zippers. As illustrated in the multiple sequence alignment presented in Appendix A, there is substantial homology to other Rad50 proteins across the entire length of SEQ ID NO: 2. Therefore, the Applicant has established a credible utility for the sequences of the present invention.

While Bork (Genome Research 10:398-400, 2000) certainly wishes to warn about the potential limits to extrapolating the data of high-throughput technologies which automatically annotate genomic sequencing efforts, he does not state that

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computer-based homology searches are invalid or questionable. In fact, on page 400, second column, second paragraph Bork states " However there is still no doubt that sequence analysis is extremely powerful and that the generation of hypotheses derived by computational methods will be more and more often the first successful step in the design of experiments. If 70% of such experiments were successful, the speed of scientific discoveries would grow exponentially."

The Applicants also respectfully draw the Examiner's attention to the Utility Examination Guidelines, Official Gazette, January 30, 2001 which state "... when a patent application claiming a nucleic acid asserts a specific, substantial, and credible utility, and bases the assertion upon homology to existing nucleic acids having an accepted utility, the asserted utility must be accepted by the examiner unless the Office has sufficient evidence or sound scientific reasoning to rebut such an assertion." The Guidelines further state "[A] 'rigorous correlation' need not be shown in order to establish practical utility; 'reasonable correlation' is sufficient." *Fujikawa v. Wattanasin*, 93 F.3d 1559, 1565, 39 USPQ2d 1895, 1900 (Fed. Cir. 1996).

The Examiner cites Lazar et al. (*Mol Cell Biol* 1998 8(3):1247-1252), and Broun et al. (*Science* 1998 282:131-133), which provide examples of very specific limited amino acid changes which result in elimination or alteration of the experimental protein's catalytic activity.

There are usually many positions within the primary sequence of a protein where substitution has little or no effect on the protein's activity, there are even cases where these sites are also part of a binding domain or active site. There are even cases where substitution of a particular amino acid can increase catalytic activity. As was stated earlier, the invention is directed to compositions of Rad50 and its activities, non-functional embodiments are not claimed and do not eliminate the utility of the function embodiments set forth in the claims.

Applicants believe that the present invention has a well-established utility for which they have proposed specific, substantial and credible uses in the present

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application. Applicants have properly addressed by argument and amendment the grounds for the rejection of originally filed claims 1-18 under 35 U.S.C. §101 as it would apply to pending claims 2-8, and 12-15, and respectfully request that the rejection of the claims under 35 U.S.C §101 be withdrawn.

**Rejections under 35 U.S.C. §112, first paragraph – Utility:**

As the Applicants have responded to the utility rejection under 35 U.S.C. §101, the concomitant rejection of claims 1-8 under 35 U.S.C. §112, first paragraph based on a lack of utility should be withdrawn and not applied to pending claims 2-8, and 12-15.

**Rejections under 35 U.S.C. §112, first paragraph – Written Description:**

Claims 1-8 are rejected under 35 U.S.C. §112, first paragraph as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. This rejection will be discussed as it pertains to original claims 2-8, and new claims 12-15.

The Examiner states: "Claim 1, part (c) is drawn to a polynucleotide having sequence amplified from a *Zea mays* nucleic acid library. No specific chemical or physical characteristics were disclosed for other polynucleotide sequences having sequence amplified from a *Zea mays* nucleic acid library. The claim encompasses undiscovered genes and undisclosed regions of *Zea mays* nucleic acid library outside of SEQ ID NO: 1 which applicant is not in possession of at the time of filing."

Claim 1 was cancelled. Original claim 1, part (c) is presented as new claim 13. The rejection will be discussed as it may be applied to new claim 13.

Claim 13 claims "A polynucleotide amplified from a *Zea mays* nucleic acid library using primers which selectively hybridize, under stringent hybridization

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conditions, to loci within a polynucleotide of SEQ ID NO: 1, wherein the polynucleotide encodes a polypeptide with Rad50 activity.”

Applicants respectfully disagree that no specific chemical and physical characteristics are disclosed. The chemical and physical characteristics include the disclosure of the full-length sequence of SEQ ID NO: 1, and the limitations that the polynucleotide be amplified from a Zea mays nucleic acid library, the primers used must selectively hybridize under stringent conditions, the primers must hybridize to loci within SEQ ID NO: 1. Claim 13 also states the amplified polynucleotide must encode a polypeptide with Rad50 activity.

Applicants clearly define amplified on page 4, lines 10-12; selectively hybridizes on page 13, lines 3-9; and stringent hybridization conditions on page 13, line 30 – page 15, line 16. Applicants provide guidance regarding amplification of polynucleotides on page 24, line 15 – page 26, line 10 and page 35, line 29 – page 36, line 19; construction of nucleic acid libraries on page 32, line 11 – page 35, line 9, and Example 1 on pages 59-60. Claim 13 clearly claims the amplification primers used must selectively hybridize under stringent conditions to loci **within** SEQ ID NO: 1.

Given the disclosure of a full-length maize Rad50 polynucleotide in SEQ ID NO: 1, guidance on amplification and nucleic acid library construction, and the clearly defined parameters of claim 13, the subject matter of claims 2-8, and 12-15 was reasonably conveyed to one of skill in the art and indicated the Applicants had possession of the claimed invention at the time of filing. Therefore, it is respectfully requested that the rejection of claims under 35 U.S.C. §112, first paragraph be withdrawn.

**Rejections under 35 U.S.C. § 102:**

Claims 1-8 have been rejected under 35 U.S.C. § 102(b) as being anticipated by Boudet et al. (US Patent 5,451,514).

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The Examiner asserts "The claims read on a polynucleotide with 2-bases, since any two bases would hybridize and would be complementary to the claimed polynucleotide."

Claim 1 was cancelled and rewritten as new claims 12-15. Original claim 1, part (d) is now presented as claim 14. Original claim 1, part (f) is not presented as claim 12, part (d). The rejection will be addressed as it may apply to these new claims.

The Applicants respectfully disagree that the claims encompass 2 nucleotide fragments. Sequences of only two nucleotides in length would not even **anneal** to the nucleic acid of the present invention under most conditions, much less **selectively hybridize** to the nucleic acid of the present invention as it is defined on page 13, lines 3 - 9 under **stringent conditions** as described on pages 13, line 30 - page 15, line 16 of the specification. Using the quick calculation for melting temperature ( $T_m$ ) of 4° C for every G or C nucleotide, or 2° C for every A or T nucleotide (Wallace formula), one can quickly calculate the approximate maximum  $T_m$  for a two nucleotide sequence to be 8° C, annealing temperature is generally calculated as 5° C lower than the  $T_m$ , or 3° C in this case. It is apparent that subsequences of only 2 nucleotides in length are not capable of annealing to, much less selectively hybridizing with, the nucleic acid of the present invention, therefore the rejection of claim 1 (d) and (f) should be withdrawn and not applied to new claims 12 and 14.

The Applicants respectfully traverse the rejection under 35 U.S.C. § 102(b). As it is stated in the MPEP 2131 page 2100-54 "To anticipate a claim, the reference must teach every element of the claim. 'A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference.'"

Boudet et al do not disclose a polynucleotide which encodes a polypeptide with Rad50 activity, or a polynucleotide that selectively hybridizes to SEQ ID NO: 1,

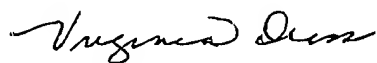
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or a polynucleotide which is fully complementary to a polynucleotide which encodes a polypeptide with Rad50 activity. Therefore, Boudet et al does not anticipate the claims and the rejection under 35 U.S.C. § 102(b) should be withdrawn.

### CONCLUSION

In light of the foregoing remarks and amendments, withdrawal of the outstanding rejections and allowance of all of the remaining claims is respectfully requested.

Respectfully submitted,



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### VERSION WITH MARKINGS TO SHOW CHANGES MADE

The Applicants have used underlining to denote additions to the original text and square brackets [ ] to denote deletions of the original text.

#### In the Title:

The title found on the cover page has been amended as follows:

[Maize] Rad50 Orthologue and Uses Thereof

#### In the Specification:

Paragraph beginning at line 18 of page 2 has been amended as follows:

The present invention describes the maize Rad50 protein, which clearly possesses features characteristic of other Rad50 proteins, and has a calculated molecular weight of ~152.5 kDa. The maize Rad50 protein is characterized by the presence of an ATP binding site in the N-terminal region, a second nucleotide binding site in the C-terminal region, putative nuclear localization signals, and heptad-repeats. The presence of extensive leucine zipper structures appears to be another striking feature of the Rad50 proteins. These are also found in the maize Rad50 protein and are indicated in **bold** in [Figure 1] Example 4. The present invention also describes a maize Rad50 polynucleotide sequence. The maize Rad50 orthologue of the present invention was used as a probe to map the maize RAD50 gene(s) to the short arm of chromosome 4.

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Paragraph beginning at line 9 of page 17 has been amended as follows:

Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information [(<http://www.ncbi.nlm.nih.gov/>)]. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length  $W$  in the query sequence, which either match or satisfy some positive-valued threshold score  $T$  when aligned with a word of the same length in a database sequence.  $T$  is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters  $M$  (reward score for a pair of matching residues; always  $> 0$ ) and  $N$  (penalty score for mismatching residues; always  $< 0$ ). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity  $X$  from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters  $W$ ,  $T$ , and  $X$  determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength ( $W$ ) of 11, an expectation ( $E$ ) of 10, a cutoff of 100,  $M=5$ ,  $N=-4$ , and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength ( $W$ ) of 3, an expectation ( $E$ ) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

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Paragraph beginning at line 8 of page 62 has been amended as follows:

Gene identities were determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1990) J. Mol. Biol. 215:403-410[; see also [www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)]) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm. The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. Nature Genetics 3:266-272 (1993)) provided by the NCBI. In some cases, the sequencing data from two or more clones containing overlapping segments of DNA were used to construct contiguous DNA sequences.

The Abstract beginning at line 1 of page 67 has been amended as follows:

#### ABSTRACT OF THE DISCLOSURE

The invention provides isolated [maize] Rad50 nucleic acids and their encoded proteins. The present invention provides methods and compositions relating to altering Rad50 levels in plants. The invention further provides recombinant expression cassettes, host cells, transgenic plants, and antibody compositions.

#### In the Claims:

Claims 1 and 9-11 have been cancelled without prejudice.

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Claims 2, 3 and 4 have been amended as follows:

2. (Amended) A recombinant expression cassette, comprising a member of claim [1] 12 operably linked[, in sense or anti-sense orientation,] to a promoter.
3. (Amended) A host cell comprising a polynucleotide of claim [2] 12.
4. (Amended) A transgenic plant comprising a recombinant expression cassette [of claim 2] comprising a polynucleotide of claim 12.

New claims 12-15 have been added as follows:

12. An isolated polynucleotide encoding a polypeptide with Rad50 activity comprising a polynucleotide selected from the group consisting of:
  - (a) a polynucleotide having at least 80% sequence identity over the entire length of the reference sequence, as determined by the GAP program under default parameters, to a polynucleotide of SEQ ID NO: 1;
  - (b) a polynucleotide encoding a polypeptide of SEQ ID NO: 2;
  - (c) a polynucleotide of SEQ ID NO: 1;
  - (d) a polynucleotide which is fully complementary to a polynucleotide of (a), (b), or (c).
13. A polynucleotide amplified from a *Zea mays* nucleic acid library using primers which selectively hybridize, under stringent hybridization conditions, to loci within a polynucleotide of SEQ ID NO: 1, wherein the polynucleotide encodes a polypeptide with Rad50 activity.

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14. A polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 0.1X SSC at 60°C, to a polynucleotide of SEQ ID NO: 1.
15. A polynucleotide comprising at least 30 contiguous nucleotides from a polynucleotide of claim 12.



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**1: AAD15407. putative RAD50 DN...**[gi:4263721] Nucleotide, Related Sequences, PubMed, Taxonomy, BLink, LinkOut

LOCUS AAD15407 1292 aa linear PLN 05-APR-2000  
DEFINITION putative RAD50 DNA repair protein [Arabidopsis thaliana].  
ACCESSION AAD15407  
PID g4263721  
VERSION AAD15407.1 GI:4263721  
DESOURCE locus AC006223 accession AC006223.3  
KEYWORDS  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (residues 1 to 1292)  
AUTHORS Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.,  
Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,  
Feldblum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,  
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L.,  
Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,  
Goodman,H.M., Somerville,C.R., Copenhagen,G.P., Preuss,D.,  
Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and  
Venter,J.C.  
TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana  
JOURNAL Nature 402 (6763), 761-768 (1999)  
MEDLINE 20083487  
PUBMED 10617197  
REFERENCE 2 (residues 1 to 1292)  
AUTHORS Lin,X.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9/12  
Medical Center Dr., Rockville, MD 20850, USA  
COMMENT Method: conceptual translation.  
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ORIGIN

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Revised: October 24, 2001.

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Save

Text

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1: AF168748. Arabidopsis thaliana [gi:7110147]

Related Sequences, Protein, PubMed, Taxonomy, LinkOut

LOCUS AF168748 4305 bp mRNA linear PLN 04-MAY-2001  
DEFINITION Arabidopsis thaliana DNA repair-recombination protein (RAD50) mRNA, complete cds.  
ACCESSION AF168748  
VERSION AF168748.1 GI:7110147  
KEYWORDS .  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 4305)  
AUTHORS Gallego,M.E., Jeanneau,M., Granier,F., Bouchez,D., Bechtold,N. and White,C.I.  
TITLE Disruption of the Arabidopsis RAD50 gene leads to plant sterility and MMS sensitivity  
JOURNAL Plant J. 25 (1), 31-41 (2001)  
MEDLINE 21097002  
PUBMED 11169180  
REFERENCE 2 (bases 1 to 4305)  
AUTHORS Gallego,M.E., Nagpal,P., Quatrano,R. and White,C.I.  
TITLE The RAD50 homolog of Arabidopsis  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 4305)  
AUTHORS Gallego,M.E., Nagpal,P., Quatrano,R. and White,C.I.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUL-1999) UMR 6547 - CNRS, Universite Blaise Pascal, 24, Ave. des Landais, Aubiere 63170, France  
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1: X14814. Yeast RAD50 gene ...[gi:4272]

Related Sequences, Protein, PubMed, Taxonomy

LOCUS SCRAD50 4775 bp DNA linear PLN 12-SEP-1993  
DEFINITION Yeast RAD50 gene for 153 kD protein.  
ACCESSION X14814  
VERSION X14814.1 GI:4272  
KEYWORDS DNA repair; DNA-binding protein; meiotic recombination; RAD50 gene.  
SOURCE baker's yeast.  
ORGANISM *Saccharomyces cerevisiae*  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
REFERENCE 1 (bases 1 to 4775)  
AUTHORS Alani, E.  
TITLE Direct Submission  
JOURNAL Submitted (21-MAR-1989) Alani E., Harvard University, 7 Divinity  
Avenue, Cambridge MA 02138, U S A  
REFERENCE 2 (bases 1 to 4775)  
AUTHORS Alani, E., Subbiah, S. and Kleckner, N.  
TITLE The yeast RAD50 gene encodes a predicted 153Kd protein containing a  
purine nucleotide binding domain and two large heptad repeat  
regions  
JOURNAL Genetics 112, 47-57 (1989)  
REFERENCE 3 (bases 1 to 4775)  
AUTHORS Raymond, W.E. and Kleckner, N.  
TITLE Expression of the *Saccharomyces cerevisiae* RAD50 gene during  
meiosis: steady-state transcript levels rise and fall while  
steady-state protein levels remain constant  
JOURNAL Molecular & general genetics : MCG. 238 (3), 390-400 (1993)  
MEDLINE 93261422  
PubMed 8492807  
COMMENT Data kindly reviewed (25-SEP-1989) by Alani E.  
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misc feature

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Add to Clipboard

1: Z75312. C.elegans mRNA fo...[gi:2687854]

Related Sequences, Protein, Taxonomy, LinkOut

LOCUS CERAD50 4121 bp mRNA linear INV 11-DEC-1997  
 DEFINITION C.elegans mRNA for RAD50.  
 ACCESSION Z75312  
 VERSION Z75312.1 GI:2687854  
 KEYWORDS RAD50.  
 SOURCE Caenorhabditis elegans.  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 Rhabditoides; Rhabditidae; Peloderinae; Caenorhabditis.  
 REFERENCE 1 (bases 1 to 4121)  
 AUTHORS Offenberg, H.H. and Heyting, C.  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 4121)  
 AUTHORS Offenberg, H.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-JUL-1996) Offenberg H.H., Agricultural University,  
 Genetics, Dreyenlaan 2, Wageningen, 6703 HA The Netherlands

FEATURES Location/Qualifiers  
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Revised: October 24, 2001.

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Structure

PopSet

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1: U63139. Homo sapiens Rad5...  
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LOCUS HSU63139 5892 bp mRNA linear PRI 07-JUL-1999

DEFINITION Homo sapiens Rad50 (Rad50) mRNA, complete cds.

ACCESSION U63139

VERSION U63139.1 GI:1518805

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5892)

AUTHORS Dolganov, G.M., Maser, R.S., Novikov, A., Tosto, L., Chong, S.,  
Bressan, D.A. and Petrini, J.H.TITLE Human Rad50 is physically associated with human Mrell:  
identification of a conserved multiprotein complex implicated in  
recombinational DNA repair

JOURNAL Mol. Cell. Biol. 16 (9), 4832-4841 (1996)

MEDLINE 96347553

PUBMED 8756642

REFERENCE 2 (bases 1 to 5892)

AUTHORS Dolganov, G.M., Maser, R.S., Novikov, A., Tosto, L., Chong, S.,  
Bressan, D.A. and Petrini, J.H.J.

TITLE Direct Submission

JOURNAL Submitted (09-JUL-1996) Human Genetics, Genelabs Technologies,  
Inc., 505 Penobscot Drive, Redwood City, CA 94063, USA

FEATURES Location/Qualifiers

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Revised: October 24, 2001.

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1: Z75311. H.sapiens mRNA fo...[gi:2687852]

Related Sequences, OMIM, Protein, Taxonomy, LinkOut

LOCUS HSRAD50 4123 bp mRNA linear PRI 11-DEC-1997

DEFINITION H.sapiens mRNA for RAD50.

ACCESSION Z75311

VERSION Z75311.1 GI:2687852

KEYWORDS RAD50.

SOURCE human.

ORGANISM Homo sapiensEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4123)

AUTHORS Offenberg, H.H.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 4123)

AUTHORS Offenberg, H.H.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-1996) Offenberg H.H., Agricultural University,  
Genetics, Dreyenlaan 2, Wageningen, 6703 HA The Netherlands

FEATURES

Location/Qualifiers

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Revised: October 24, 2001.

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1: NM\_022246. Rattus norvegicus...[gi:11560047]

Related Sequences, Protein, PubMed, Taxonomy, LinkOut

LOCUS NM\_022246 4444 bp mRNA linear ROD 06-DEC-2000

DEFINITION Rattus norvegicus RAD50 homolog (S. cerevisiae) (Rad50), mRNA.

ACCESSION NM\_022246

VERSION NM\_022246.1 GI:11560047

KEYWORDS

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 4444)

AUTHORS Lanson, N.A. Jr., Egeland, D.B., Royals, B.A. and Claycomb, W.C.

TITLE The MRE11-NBS1-RAD50 pathway is perturbed in SV40 large T  
antigen-immortalized AT-1, AT-2 and HL-1 cardiomyocytes

JOURNAL Nucleic Acids Res. 28 (15), 2882-2892 (2000)

MEDLINE 20368653

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final  
NCBI review. The reference sequence was derived from AF218576.1.

FEATURES

Location/Qualifiers

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misc feature 990..1958

/note="filament; Region: Intermediate filament proteins"

misc feature 1635..2144

/note="V\_ATPase\_sub\_a; Region: V-type ATPase 116kDa subunit family"

misc feature 3705..3986

/note="ABC\_tran; Region: ABC transporter"

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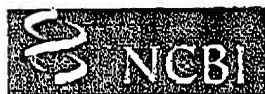
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Revised: October 24, 2001.

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Structure

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1: U66887. Mus musculus DNA ...[gi:1575574] ProbeSet, Related Sequences, Protein, PubMed, Taxonomy, LinkOut

LOCUS MMU66887 5088 bp mRNA linear ROD 15-NOV-1996  
DEFINITION Mus musculus DNA repair protein RAD50 (RAD50) mRNA, complete cds.  
ACCESSION U66887  
VERSION U66887.1 GI:1575574  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 5088)  
AUTHORS Kim,K.K., Daud,A.I., Wong,S.C., Pajak,L., Tsai,S.C., Wang,H.,  
Henzel,W.J. and Field,L.J.  
TITLE Mouse RAD50 has limited epitopic homology to p53 and is expressed  
in the adult myocardium  
JOURNAL J. Biol. Chem. 271 (46), 29255-29264 (1996)  
MEDLINE 97067183  
REFERENCE 2 (bases 1 to 5088)  
AUTHORS Kim,K.K., Daud,A.I., Wong,S.C., Pajak,L., Tsai,S.C., Wang,H.,  
Henzel,W.J. and Field,L.J.  
TITLE Direct Submission  
JOURNAL Submitted (14-AUG-1996) Medicine, Indiana University, Krannert  
Institute of Cardiology, 1111 West 10th Street, Indianapolis, IN  
46202-4800, USA

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# APPENDIX A

## !!AA\_MULTIPLE\_ALIGNMENT 1.0 PileUP

Symbol comparison table: genrundata:blosum62.cmp CompCheck: 1102

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FORMATTING: identical residue

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 U66887aa Q R Q T G G K K E C Q T E L K Y E K Q N K K A C E R A I S K E A Q L A S E I  
 AAD15407aa e i k e f l k l e n l o t k d a a y k l r e s i a d d q e s k v g m  
 AF168748aa e i k e f l k l e n l o t k d a a y k l r e s i a d d q e s k v o m  
 1116sid2 e i k e f l k l e n l o t k d a a y k l r e n i a d d q e k d s k s o m  
 X14814aa K S K G M S V E K L L Q S E H K L D K E R K A L N T H O L Q T K I Q Y N E E  
 Z75312aa K K V L D F K K E Q T H E S K Q L Y E T H V R D K L V A R Q N Q E E C E R K I S K R K E E T

251 300

U63139aa K S Y E N E D P L K N R K E E H N L S K M L D N E K A L D R K Q E K D S E L E E  
 Z75311aa K S Y E N E D P L K N R K E E H N L S K M L D N E K A L D R K Q E K D S E L E E  
 NM022246aa K A Y E N E E P L K N R K E E H N L S K M R L D N E K A L D R K Q E K D S E L E Q  
 U66887aa R S Y E E P L K N R K E E H N L S K M L D N E K A L E R K Q E K D S E L E Q  
 AAD15407aa l e l e t s q k v a e h k e m m l k l r l o d q s i k t e r s t l f k e q r q y a  
 AF168748aa L E L E T S Q K V A E H K E M M L K L R L O D Q S I K T E R S T L F K E Q R Q Y A  
 1116sid2 Q L A T C G T E T L M E T S L D E L R R L O G O I K A E R S T I L T O O H E K L A  
 X14814aa S E E S Q N E I T E K S D K F K S N Q F O L S K N L K N T L S D O V K R L S N  
 Z75312aa E I K E K A N G Q K E E M R T S H E L E D T L T S F K K T E L E R Q N L K K O L S L I R V

301 350

U63139aa K E K V F Q G E E O L N L Y H N H Q R T . R E K E R K V D C H R K L N K E S R I N  
 Z75311aa K E K V F Q G E E O L N L Y H N H Q R T . R E K E R K V D C H R K L N K E S R I N  
 NM022246aa K E K V F Q G E E O L N L Y H N H Q R T . R E K E R V D C O R K L K E R I N  
 U66887aa K E K V F Q G E E O L N L Y H N H Q R T . R E K E R V D C O R K L N K E R I N  
 AAD15407aa a l p e e n e d t i e e l k e w k e f e e r . a l l g t k i r k e r e m v d t e t i s s i h  
 AF168748aa A L P E E N E D T I E E L K E W K E F E E R . A L L G T K I R K E R E M V D T E T I S S I H  
 1116sid2 A L S R E N E D T I E E L M E W Q K F E E R . A L L E T K I K I V R D M D E F Y S S I S  
 X14814aa D . I L L K P L O N L L N E S K V . M D K N N Q R D L E T E S S L K D R O S S I Q  
 Z75312aa . . . P Y F G E E E L K R E I E E E R G S E G R S Y G E E R Q K G K N N Q E R Q E I S



351 400

U63139aa	QEKSEELVFEQ	GELQLOADRH	QEHIRARDSL	TQSAATQLE	LDGFERGPF
Z75311aa	QEKSEELVFEQ	GELQLOADRH	QEHIRARDSL	TQSAATQLE	LDGFERGPF
NM022246aa	QERSEELVFEQ	GELQLOADRH	QEHIRARDSL	TQSAATHLE	LDGFERGPF
U66887aa	QEKSEELVFEQ	GELQLOADRH	QEHIRARDSL	TQSAATHLE	LDGFERGPF
AAD15407aa	naknymle	sklqteaah	llknerdst	lgniffhyn	lgnvstpf
AF168748aa	NAKNYMLE	SKLOTEAAH	LKNERDST	QNIFFHYN	LGNVSTPF
1116sid2	KQNSETHET	GKLOAEADAH	LKHERDSD	EKNICTKHN	LGPVPEHPF
X14814aa	SLSNSHRRQ	GEAEAGK	EKN	NHLSSL	KEAFQHKFG
Z75312aa	QKKSEFENR	SSKAEVIHC	QKYLRL	ENRELD	...EHDADI

401 450

U63139aa	ERQIKNFHKL	ERQEGE.A	KTANQIMNDF	AKETLKQKQ	D.....E
Z75311aa	ERQIKNFHKL	ERQEGE.A	KTANQIMNDF	AKETLKQKQ	D.....E
NM022246aa	ERQIKNFHEL	ERQERE.A	KTASQILLSDE	TDEALKQKQ	D.....E
U66887aa	ERQIKNFHEL	ERQERE.A	KTASQILLSDE	TDEALKQKQ	D.....E
AAD15407aa	tgvnltnr	ikr	lgelemol	ldkksneta	lstawdcy
AF168748aa	TGVNLTNR	IKR	LGELEMOI	LDKKSNETA	LSTAWDCY
1116sid2	NVAALTNR	IKR	LSLENDL	LDKKSNEOQ	LEVWKHY
X14814aa	..QVNHMSQ	FKAFISQDLT	DT	DQFAKE	QLNETNLSDL
Z75312aa	DIEIDAIT	KIGMSDKA	RM	KNCA	QSNLR

451 500

U63139aa	IRDKSGGR	ITE.LKSEI	S..KQNELK	NVKY.LQQLE	GSSDR.LE
Z75311aa	IRDKSGGR	ITE.LKSEI	S..KQNELK	NVKY.LQQLE	GSSDR.LE
NM022246aa	IRDKSGGR	MTE.LKTEI	S..KQTEL	NVRN.LQQLE	GSSDR.LE
U66887aa	IRDKSGGR	ITE.LKTEI	S..KQSEL	HVRS.LQQLE	GSSDR.LE
AAD15407aa	ardksa	gkr	ldkdk	mgis	hiefefef
AF168748aa	ANDKSA	QKR	KDEIK	MGIS	RIE
1116sid2	INARSG	QIQ	KIES	SGIL	E
X14814aa	EYNKKRSK	LH.DSEELA	EK	KSF	SLS
Z75312aa	NEKVK	E	EQLKFKIK	QCONATAGM	LL

501 550

U63139aa	QELIKAERE	S.AEKNNSVE	TLKME	ISLO	NEKADLRT
Z75311aa	QELIKAERE	S.AEKNNSVE	TLKME	ISLO	NEKADLRT
NM022246aa	QELTKAERE	S.AEKNSSIE	TLK	E.L.LO	NEKADLRT
U66887aa	QELTKAERE	S.AEKNSSIE	TLK	E.MSLO	NEKADLRT
AAD15407aa	elqge	gskkqnser	g	skleeka	heyslehti
AF168748aa	EREQGE	ERKTKQNSER	G	SKLEOKQ	HEYSLEHKT
1116sid2	EREHQE	ERKTLALGER	DY	SITSOKR	HEYSLEHKT
X14814aa	.NLTYKEK	QSWESENIIP	KLNQKTEEK	NE	IILE
Z75312aa	ENALTECK	K	.....E	KYLKQ	DILK

[illegible]

751 800

U63139aa LK TESELKK KKKRRDE LG LVP RQ I D EKE . . KETPE LRNKL VNR  
 Z75311aa LK TESELKK KKKRRDE LG LVP RQ I D EKE . . KETPE LRNKL VNR  
 NM022246aa LK TESELKK KKKRRDE LG LVP RQ I D EKE . . KETPE LRNRL SVN  
 U66887aa LK TESELKK KKKRRDE LG LVP RQ I D EKE . . KETPE LRNRL SVN  
 AAD15407aa LKALA ESEN A EGOOLDK LR EYSK TTT . . EITPL AEKTE ETE  
 AF168748aa LKALA ESEN A EGOOLDK LR EYSK TTT . . EITPL AEKTE ETE  
 1116sid2 LKALA ESEN A EGOOLDK LR EYSK TTT . . EITPL AEKTE ETE  
 X14814aa LKD QNEK . . . . EYHS LRL EKHI T ENSINEKDN QKCEKAKE  
 Z75312aa QEE EKLVS K LK . EE II EGOA . NE LQIVKE KE VREKNRKL

801 850

U63139aa DIQRLK DI QET LGT M P E AKVCE TD VTI RF QME KD E K  
 Z75311aa DIQRLK DI QET LGT M P E AKVCE TD VTI RF QME KD E K  
 NM022246aa DIQRLK DI QET LGT M P E AKVCE TD VTI RF QME KD E K  
 U66887aa DIQRLK DI QET LGT M P E AKVCE TD VTI RF QME KD E K  
 AAD15407aa lga ke al a g sa q k a a d e l l o p . l na d r i f q e v s y q k q  
 AF168748aa LGOK EALD E E SAQ K AD D EAL OP . L NADRI FQETVSYQKQ  
 1116sid2 DESOK AFO DELG LAHY MD D EAL OP . T TIDRH VHEEQOLVKE  
 X14814aa TKTSKSKL E EVDS K K D LA E E RELI KFTYL EKE KDIENS  
 Z75312aa MAEEKSNLS KNEKQETV AKLKLAD L QTDVGVTOOL YEQTEENEKR

851 900

U63139aa AQQAAKQG IDLD . QQ QEK EKH KLDT SSK LNRKLIQDQ  
 Z75311aa AQQAAKQG IDLD . QQ QEK EKH KLDT SSK LNRKLIQDQ  
 NM022246aa AQQAAKQG VLDL . QQ QEK EKH KLDT SSK LNRKLIQDQ  
 U66887aa AQQAAKQG VLDL . QQ QEK EKH KLDT SSK LNRKLIQDQ  
 AAD15407aa EDEYKGF RGLSVK E E GSELSSGS AKHGE KLDDQIYE  
 AF168748aa EDEYKGF RGLSVK E E GSELSSGS AKHGE KLDDQIYE  
 1116sid2 EDEYALDS SGRGVK E E QLEL FLO DTLIVE DLDDQHRM  
 X14814aa SKT SEE SI YNTSEDG QT DELRDQQR MND RELRK T SLOQMEKD  
 Z75312aa YQEVSESDG SDGLSY . . . . . ERKKVE D DEYRK V QEG ELQKCS

901 950

U63139aa EQ QHLKSTT NEL SEK QI S . . . NTORR QOLEEQTVEL TEVQSHYRE  
 Z75311aa EQ QHLKSTT NEL SEK QI S . . . NTORR QOLEEQTVEL TEVQSHYRE  
 NM022246aa EQ QHLKS T NEL SEK QI . . . NTORR QOMEEQTVEL TEVQSNRE  
 U66887aa EQ QHLKS T NEL SEK QI . . . NTORR QOMEEQSVEL TEVQSNRE  
 AAD15407aa rd cl a a n h a v r e e k a k . . . n l r d v t k e e l e r l a e e k s o l d  
 AF168748aa RD SCLOARN HAVREERAK . . . NLRDV TK E E ERL AEEKSOLD  
 1116sid2 ED SSAQVRA HNAREEKVA S . . . S LERF OK E E E V L L A E E K E O L I E  
 X14814aa EK RENS RMI NLI EKE TV SEIESSTQK QNI S RSK RENIND DSR  
 Z75312aa E RNKLOS L NELGTH VSL GEAA . . . QA GAFAEQETK IKEIQEC TA

951 1000

U63139aa	IKDAK.EQ S	PIETTLEKFQ	OEKEELIHK	NTSNKIAQ	LN IKEK KN
Z75311aa	IKDAK.EQ S	PIETTLEKFQ	OEKEELIHK	NTSNKIAQ	LN IKEK KN
NM022246aa	IKDAK.EQ N	PIETIALEKFQ	OEKEELIHK	NTSNKMAQ	IN IKEK KN
U66887aa	IKDAK.EQ S	PIETIALEKFQ	OEKEELIHK	HTSNKMAQ	IN IKEK KN
AAD15407aa	VKYLT.FLG	PIETIALEKFQ	OEKEELIHK	HTSNKMAQ	IN IKEK KN
AF168748aa	VKYLT.FLG	PIETIALEKFQ	OEKEELIHK	HTSNKMAQ	IN IKEK KN
1116sid2	KYLLE.FLD	PIETIALEKFQ	OEKEELIHK	HTSNKMAQ	IN IKEK KN
X14814aa	VKELE.ARI	PIETIALEKFQ	OEKEELIHK	HTSNKMAQ	IN IKEK KN
Z75312aa	ISQKRNE.DP	PIETIALEKFQ	OEKEELIHK	HTSNKMAQ	IN IKEK KN

1001 1050

U63139aa	HGYMKD.TEN	YIQDGKDDYK	KQ.KETELK	...VIQES	ECEKHKE.IN
Z75311aa	HGYMKD.TEN	YIQDGKDDYK	KQ.KETELK	...VIQES	ECEKHKE.IN
NM022246aa	HGYMKD.TEN	YIQDGKDDYK	KQ.KETELK	...VVIQES	ECEKHKE.IN
U66887aa	HGYMKD.TEN	YIQDGKDDYK	KQ.KETELK	...VAVQES	ECEKHKE.IN
AAD15407aa	ILASYKND	CFTRHALLK	GE.LDGE	QRISDSOLO	SCEAKKE
AF168748aa	ILASYKND	CFTRHALLK	GE.LDGE	QRISDSOLO	SCEAKKE
1116sid2	ILASYKND	CFTRHALLK	GE.LDGE	QRISDSOLO	SCEAKKE
X14814aa	FQTYNE.VD	FEAKGFDELO	TTIKELK	...L	ELKEQLDLKS
Z75312aa	RKS.FKKQE	...GGCEQ	LMDKENN	...ATLN	SE ENQQOKRFE

1051 1100

U63139aa	E.RLM.QD	DTOKIQERW	QDNLTLRKRN	E.KE.E...	BERKQHLKE
Z75311aa	E.RLM.QD	DTOKIQERW	QDNLTLRKRN	E.KE.E...	BERKQHLKE
NM022246aa	KE.GTM.QD	DTOKIQERW	QDNLTLRKRN	E.KE.E...	BERKQHLKE
U66887aa	KE.GTM.QD	DTOKIQERW	QDNLTLRKRN	E.KE.E...	BERKQHLKE
AAD15407aa	GELN.NK	RNDOL.RNT	QDNLTLRKRN	E.KE.E...	BERKQHLKE
AF168748aa	GELN.NK	RNDOL.RNT	QDNLTLRKRN	E.KE.E...	BERKQHLKE
1116sid2	GELN.NK	RNDOL.RNT	QDNLTLRKRN	E.KE.E...	BERKQHLKE
X14814aa	NEVNNEEKRL	ADSNNEE	KONLELIELK	Q.QHES	SRL...QN
Z75312aa	E.RS....F	DSSHORESI	KD.LTRMIIE	NK.KELKT	A.FGO.NED

1101 1150

U63139aa	GO.QV.QMK	HO.LEENI	N.KRNHNLAL	GRQKGEEET	IHFKKEL.EP
Z75311aa	GO.QV.QMK	HO.LEENI	N.KRNHNLAL	GRQKGEEET	IHFKKEL.EP
NM022246aa	GO.QV.QMKN	HO.LEENI	T.KRNHSLAL	GRQKGEEET	IHFKKEL.EP
U66887aa	GO.QV.QMKN	HO.LEENI	T.KRNHSLAL	GRQKGEEET	IHFKKEL.EP
AAD15407aa	GG.AE...A	VILRE	RLSELNRCR	GT.SVYESSI	SKNVELKQ
AF168748aa	GG.AE...A	VILRE	RLSELNRCR	GT.SVYESSI	SKNVELKQ
1116sid2	GG.AE...A	VILRE	RLSELNRCR	GT.SVYESSI	SKNVELKQ
X14814aa	AEAERDKYQE	ESLRLTRFE	ELSENAGKL	GE.KQLON	DSLTHQL
Z75312aa	...RITEQKQ	AYN.LQELR	LGNEEV.IY	TQ.QEYK	K KIAEAKLSTK

1151

U63139aa	QASEYR	EMMV	TE	VNKDLDIY	KALDQAMF	HSMKMEETNK
Z75311aa	QASEYR	EMMV	TE	VNKDLDIY	KALDQAMF	HSMKMEETNK
NM022246aa	QASEYR	EMMV	TE	VNKDLDIY	KALDQAMF	HSMKMEETNK
U66887aa	QASEYR	EMMV	TE	VNKDLDIY	KALDQAMF	HSMKMEETNK
AAD15407aa	QYKDLKRFH	DGL	QKITE	MANKDLDRY	NALDKALMRF	HSMKMEETNK
AF168748aa	QYKDLKRFH	DGL	QKITE	MANKDLDRY	NALDKALMRF	HSMKMEETNK
1116sid2	QYKDLKRFH	DGL	QKITE	MANKDLDRY	NALDKALMRF	HSMKMEETNK
X14814aa	DYKDLKRFH	KE	ELQTRS	FVTDD	LVYS	KALDSAMF
Z75312aa	ECQNAESNYR	DAI	EAATK	E	ISDIT	YR

1200

1201

U63139aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
Z75311aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
NM022246aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
U66887aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
AAD15407aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
AF168748aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
1116sid2	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
X14814aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD
Z75312aa	ELNRSIV	RGODIY	ET	RSDADENVSA	SDKRRNMYR	VVMLKGD

1250

1251

U63139aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
Z75311aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
NM022246aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
U66887aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
AAD15407aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
AF168748aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
1116sid2	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
X14814aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI
Z75312aa	MRGRCSAGO	KVLASLIIRI	ALAETFCINC	GILALDEPTT	NLDRENIESI

1300

1301

U63139aa	AHAT	ET	K	RSQ	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
Z75311aa	AHAT	ET	K	RSQ	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
NM022246aa	AHAT	ET	K	RSQ	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
U66887aa	AHAT	ET	K	RSQ	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
AAD15407aa	AGAT	ET	IMED	RKG	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
AF168748aa	AGAT	ET	IMED	RKG	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
1116sid2	AGAT	ET	IMED	RKG	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
X14814aa	AK	ET	HN	IM	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY
Z75312aa	AK	ET	HN	IM	.....	ORNEFOLVI	THDEDEVEL	GRSEYVEKY

1350